WHAT IS CLAIMED IS:

1. A computer implemented process for developing a model which predicts the value of a single dependent variable based on the value of at least one independent variable comprising the steps of:

(a) providing a dataset containing a plurality of observations each containing a value for said dependent variable and values for said at least one independent variable;

(b) creating from said dataset of an initial generation of chromosomes each comprising a predictive model;

(c) determining a quantitative fitness measure for each chromosome in said initial generation; and

(d) creating a next generation of chromosomes by selecting a number of chromosomes from said initial generation, crossing said selected chromosomes by at least one of a cloning and a crossover technique, and mutating said chromosomes.

2. A process according to claim 1, further comprising (e) determining new fitness measures for said chromosomes in said next generation, and (f) repeating said selecting, crossing and mutating steps to create a successive generation of chromosomes.

3. A process according to claim 2, further comprising continuously repeating steps (e) and (f) for said successive generation of chromosomes to create another successive generation of chromosomes.

4. A process according to claim 1, wherein said initial generation chromosome creating step is performed using a random method.

5. A process according to claim 1, wherein said initial generation chromosome creating step is performed using a distributed method.

6. A process according to claim 1, wherein said chromosome creating step comprises forming a chromosome having a plurality of observed variable segments each formed by a plurality of genes, a plurality of interaction segments

each formed by a plurality of genes, and an intercept gene positioned after said plurality of interaction segments.

7. A process according to claim 6, further comprising limiting the number of interaction segments in each said chromosome to a fixed parameter or applying a predetermined rule to determine the number of interaction gene segments.

8. A process according to claim 6, wherein said chromosome forming step comprises forming at least one observed continuous variable gene segment so as to contain an include/exclude gene, a coefficient gene, a minimum outlier gene, a maximum outlier gene, a transformation gene, and a ranking gene.

9. A process according to claim 8, further comprising forming a plurality of observed continuous variable gene segments and using said include/exclude gene to indicate whether a variable for a particular one of said observed continuous variable segments is included in an embedded model.

10. A process according to claim 9, further comprising using said coefficient gene to identify a coefficient value

for an observed continuous variable described by the particular one of said observed variable segments.

11. A process according to claim 10, further comprising forming said coefficient gene from a plurality of binary bits and designating a number of said binary bits as a super bit where all of said bits flip under certain conditions.

12. A process according to claim 10, further comprising using said outlier genes in each said observed continuous variable segment to trim a distribution range for the observed value in said observed continuous variable segment.

13. A process according to claim 12, further comprising representing said outlier genes in a double stranded format.

14. A process according to claim 12, further comprising using said transformation gene to eliminate skewness and kurtosis from a distribution range for said observed variable in said observed continuous variable segment and

to transform said distribution range as close as possible to normality.

15. A process according to claim 6, wherein said chromosome forming step comprises forming at least one observed categorical variable segment consisting of an include/exclude gene, a contrast gene, and at least one coefficient gene.

16. A process according to claim 15, further comprising forming a plurality of observed categorical variable segments and using said include/exclude gene to indicate whether a variable for a particular one of said observed categorical variable segments is included in an embedded model.

17. A process according to claim 16, further comprising using said coefficient gene to identify a coefficient value for the observed categorical variable described by the particular one of said observed variable segments.

18. A process according to claim 17, further comprising forming said coefficient gene from a plurality of binary bits and designating a number of said binary bits as a

super bit where all of said bits flip under certain conditions.

19. A process according to claim 15, further comprising using said contrast gene to indicate a maximum number of categories allowed for a requested model.

20. A process according to claim 6, wherein said chromosome forming step further comprises forming each interaction segment to contain an include/exclude gene, a coefficient gene, a first variable gene, a second variable gene, and an operator gene.

21. A process according to claim 20, further comprising using said include/exclude gene to indicate if a particular interaction variable described by a particular interaction segment is included in the model.

22. A process according to claim 21, further comprising using the coefficient gene to indicate a coefficient value for the interaction variable described by a particular interaction segment.

23. A process according to claim 22, further comprising using said first variable gene to identify a first observed variable used to derive a value of the interaction variable.

24. A process according to claim 23, further comprising using said operator gene to select an operator used to derive an interaction value from two observed variables.

25. A process according to claim 24, wherein said operator is selected from the group consisting of addition, multiplication, subtraction, difference squared, division, and absolute difference.

26. A process according to claim 24, further comprising using said second variable gene to identify a second of two observed variables used to derive the value of the interaction variable.

27. A process according to claim 26, further comprising randomly selecting said first and second variable genes in each of said interaction segments.

28. A process according to claim 1, wherein said fitness measure determining step comprises providing a scheduler module and a plurality of fitness evaluator modules and using said scheduler module to direct one of said chromosomes in said generation to be measured to an available one of said evaluator modules.

29. A process according to claim 28, wherein said fitness measure determining step comprises selecting a fitness metric and determining a fitness rating for said one chromosome using said fitness metric.

30. A process according to claim 28, further comprising providing at least one modeler module, accumulating a fitness measure for each said chromosome in said scheduler module, and transmitting said accumulated fitness measures from said scheduler module to said at least one modeler module.

31. A process according to claim 30, further comprising performing said new generation chromosome creating step using said at least one modeler module.

32. A process according to claim 31, further comprising weighting each said chromosome in said generation and said selecting step comprising randomly selecting said weighted chromosomes.

33. A process according to claim 32, wherein said procreated step comprises selecting a crossover rate and a number of crossover points and creating two offspring chromosomes from two selected parent chromosomes using said selected crossover rate and said crossover points.

34. A system for creating a predictive model comprising:

means for creating an initial generation of chromosomes from a dataset with each chromosome in said initial generation comprising a predictive model;

means for determining a quantitative fitness measure for each chromosome in said initial generation; and

means for selecting a number of said initial generation chromosomes, for crossing the selected initial generation chromosomes by at least one of cloning and a

pure (standard) crossover technique, and for mutating the crossed chromosomes into a next generation of chromosomes.

35. A system according to claim 34, further comprising a computer and said initial generation chromosome creating means comprising at least one modeler module within said computer.

36. A system according to claim 35, further comprising a scheduler module in said computer and at least one fitness evaluator in said computer forming said means for determining a quantitative fitness measure.

37. A system according to claim 36, further comprising a plurality of fitness evaluators in said computers and said scheduler module determining which of said plurality of fitness evaluators shall determine the fitness measure for a particular one of said chromosomes.

38. A system according to claim 35, wherein said at least one modeler module also forms said means for selecting a number of initial generation chromosomes, for crossing the selected initial generation chromosomes, and for mutating the crossed chromosomes.

39. A system according to claim 35, further comprising a user interface module.

40. A system according to claim 35, further comprising a database within said computer for storing datasets and best predictive models and said at least one modeler module communicating with said database.

41. A chromosome for predicting a model comprising a plurality of observed variable segments, a plurality of interaction segments and an intercept gene.

42. A chromosome according to claim 41, further comprising said intercept gene being positioned on said chromosome after said plurality of interaction segments.

43. A chromosome according to claim 41, wherein said plurality of interaction segments is limited in number to a preset value or by a predetermined rule.

44. A chromosome according to claim 41, wherein said observed variable segments contain at least one observed continuous variable segment comprising an include/exclude

gene, a coefficient gene, a minimum outlier gene, a maximum outlier gene, a transforming gene, and a ranking gene.

45. A chromosome according to claim 44, wherein each of said outlier genes is represented in a double stranded format.

46. A chromosome according to claim 41, wherein said observed variable segments contain at least one observed categorical variable segment comprising an include/exclude gene, a contrast gene, and at least one coefficient gene.

47. A chromosome according to claim 41, wherein each of said interaction segments contains an include/exclude gene, a coefficient gene, a first variable, a second variable, and an operator.

48. A chromosome according to claim 47, wherein each of said first and second variables is randomly selected from a number of variables in a dataset.